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**A Patient with Pontocerebellar Hypoplasia Type 6: Novel *RARS2* Mutations, Comparison to
Previously Published Patients and Clinical Distinction from PEHO Syndrome**

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Abstract

Pontocerebellar hypoplasia type 6 (PCH6) is a rare infantile-onset progressive encephalopathy caused by biallelic mutations in *RARS2* that encodes the mitochondrial arginine-tRNA synthetase enzyme (mtArgRS). The clinical presentation overlaps that of PEHO syndrome (Progressive Encephalopathy with oedema, Hypsarrhythmia and Optic atrophy). The proband presented with severe intellectual disability, epilepsy with varying seizure types, optic atrophy, axial hypotonia, acquired microcephaly, dysmorphic features and progressive cerebral and cerebellar atrophy and delayed myelination on MRI. The presentation had resemblance to PEHO syndrome but sequencing of *ZNHIT3* did not identify pathogenic variants. Subsequent whole genome sequencing revealed novel compound heterozygous variants in *RARS2*, a missense variant affecting a highly conserved amino acid and a frameshift variant with consequent degradation of the transcript resulting in decreased mtArgRS protein level confirming the diagnosis of PCH6. Features distinguishing the proband's phenotype from PEHO syndrome were later appearance of hypotonia and elevated lactate levels in blood and cerebrospinal fluid. On MRI the proband presented with more severe supratentorial atrophy and lesser degree of abnormal myelination than PEHO syndrome patients. The study highlights the challenges in clinical diagnosis of patients with neonatal and early infantile encephalopathies with overlapping clinical features and brain MRI findings.

Keywords

Pontocerebellar hypoplasia type 6, *RARS2*, PEHO syndrome, progressive cerebellar and cerebral atrophy

42 Introduction

43 Pontocerebellar hypoplasia (PCH) is a group of neurodegenerative disorders with autosomal
44 recessive inheritance. Up to date 11 different subtypes have been described, with 17 causative
45 genes identified (van Dijk et al., 2018). Most of the subtypes are characterized by prenatal or
46 neonatal onset, global developmental delay and intellectual disability, microcephaly, hypoplasia
47 and variable atrophy of cerebellar cortex and/or brainstem. The specific neurological symptoms
48 and the severity of symptoms and brain loss vary between the subtypes (van Dijk et al., 2018).

49 Pontocerebellar hypoplasia type 6 (PCH6; MIM 611523) is a rare form of PCH first described in
50 2007 in three patients of a consanguineous Sephardic Jewish family (Edvardson et al., 2007). Since
51 then, altogether 32 patients in 18 families have been reported in the literature (for a detailed
52 summary of the patients and phenotypes, see Supplementary Table; Edvardson et al., 2007; Rankin
53 et al., 2010; Namavar et al., 2011; Glamuzina et al., 2012; Cassandrini et al., 2013; Kastrissianakis
54 et al., 2013; Joseph et al., 2014; Li et al., 2015; Lax et al., 2015; Nishri et al., 2016; Alkhateeb et al.,
55 2016; Ngoh et al., 2016; van Dijk et al., 2017; Luhl et al., 2016; Zhang et al., 2018). Most PCH6
56 patients present with neonatal onset, hypotonia, microcephaly, seizures, severe intellectual
57 disability with lack of developmental milestones and progressive atrophy of cerebral cortex,
58 cerebellum and pons. The majority show a respiratory chain enzyme deficiency and elevated
59 lactate levels in blood or cerebrospinal fluid (CSF). Indeed, PCH6 may be distinguished from the
60 other PCH subtypes, which are highly variable clinically and neuroradiologically, by the presence of
61 elevated lactate concentration (van Dijk et al., 2018).

62 PCH6 is caused by biallelic mutations in *RARS2*, a nuclear gene that encodes the mitochondrial
63 arginine-tRNA synthetase enzyme (mtArgRS) (Edvardson et al., 2007). Aminoacyl-tRNA synthetases
64 play a crucial role in protein translation as they catalyze the specific attachment of an amino acid

(aminoacylation) to its cognate tRNA. MtArgRS participates in the synthesis of all 13 mitochondrial-encoded proteins by charging of mitochondrial tRNA-Arg, thus being an integral part of mitochondrial protein translation machinery, participating in generation of complexes of oxidative phosphorylation system, except complex II, which has a fully nuclear origin (Ibba and Soll, 2000).

PCH6 shows clinically some resemblance to PEHO syndrome (Progressive Encephalopathy with oedema, Hypsarrhythmia and Optic atrophy; MIM 260565), characterized by neonatal hypotonia, profound psychomotor retardation, infantile spasms with hypsarrhythmia and atrophy of optic disks (Salonen et al., 1991). Patients present with typical dysmorphic features, such as narrow forehead, epicanthic folds, short nose and open mouth, and edema of the face and limbs (Somer, 1993). Neuroimaging findings include demyelination and progressive atrophy of the cerebellar cortex, brainstem and optic nerves. In the cerebellum, the inner granular layer is nearly totally absent and Purkinje cells are deformed and disaligned (Haltia and Somer, 1993).

PEHO syndrome is inherited autosomal recessively and was recently shown to be caused in Finnish patients by a homozygous missense mutation c.92C>T; p.Leu31Ser in *ZNHIT3*, a gene encoding zinc finger HIT domain-containing protein 3 (Anttonen et al., 2017). PEHO syndrome is enriched in the Finnish population with an estimated incidence of 1:74 000 (Somer, 1993) and approximately 40 diagnosed patients. In other populations it is very rare, with less than 25 reported patients (Field et al., 2003; Caraballo et al., 2011; Alfadhel et al., 2011) and only one patient with compound heterozygous mutations in *ZNHIT3* reported so far (Öunap et al., 2019). In the literature, patients with symptoms closely resembling PEHO syndrome are more commonly reported. The clinical presentation of patients with PEHO-like features, like those with PCH, is similar to that of PEHO syndrome, but optic atrophy and typical neuroradiologic findings are usually absent or there is no progression (Field et al., 2003; Longman et al., 2003; Chitty et al., 1996). Several genes underlying

88 phenotypes resembling PEHO have been described (Rankin et al., 2010; Anttonen et al., 2015;
89 Gawlinski et al., 2016; Langlois et al., 2016; Nahorski et al., 2016; Flex et al., 2016; Miyake et al.,
90 2016; Zollo et al., 2017; Chitre et al., 2018).

91 We report a patient with the initial presenting features suggestive of PEHO syndrome with typical
92 dysmorphic features, epileptic spasms, optic atrophy and severe hypotonia, but in whom whole
93 genome sequencing revealed novel compound heterozygous mutations in *RARS2*.

Materials and methods

Patient and samples

The proband was clinically examined by B.C. in Antwerp and was referred to molecular genetic analyses in Helsinki. DNA extracted from peripheral blood was obtained from the proband and both parents. Primary fibroblast cultures from the proband were available for analyses of the gene product.

An institutional review board at the Helsinki University Central Hospital approved the study. A written informed consent was obtained from the parents.

Sequencing of *ZNHIT3*

The five coding exons of *ZNHIT3* (NM_004773.3) were Sanger sequenced from genomic DNA of the proband (primer sequences available upon request). Exon 1 covering the c.8C>T, p.Ser3Leu variant was also sequenced in the parents.

Whole genome sequencing

Library preparation for the genomic DNA sample was performed using KAPA Library Preparation Kit. The sample was sequenced in three lanes of an Illumina HiSeq2500 instrument with one lane having paired-end 250-bp reads and two lanes paired-end 10-bp reads. Sequence read alignment to human reference genome (GRCh37) and variant calling (Li et al., 2009) was done as described earlier with minor modifications (Sulonen et al., 2011). Called variants were annotated using ANNOVAR (Wang et al., 2010) and filtered using in-house scripts. DELLY (Rausch et al. 2012), which assesses split-read alignments and paired-end read information to detect structural variants was used to identify any copy number changes overlapping with the *ZNHIT3* locus. Sanger sequencing

117 was performed from genomic DNA of the patient and the parents to validate the variants
118 identified by whole genome sequencing and to test segregation of the variants in the family.
119 Primer sequences are available upon request.

120

121 **Sequencing of patient cDNA**

122 Patient fibroblasts were harvested, total RNA extracted (RNeasy plus mini kit, QIAGEN) and
123 complementary DNA (cDNA) prepared (iScript cDNA synthesis kit, BioRad). Polymerase chain
124 reaction was performed using primers (sequences available upon request) binding to exons 8 and
125 14 of *RARS2* and the resulting 600-bp product covering the positions of the mutations in exons 10
126 and 11 was sequenced using standard protocols.

127

128 **Western blot analysis**

129 Protein extracts for the detection of mtArgRS, COXII or GAPDH were prepared by lysing fibroblasts
130 in RIPA buffer (Cell Signaling Technology) containing protease inhibitors (Halt, Thermo Fisher
131 Scientific). After 10 min incubation on ice the samples were centrifuged at 14 000 g for 10 min (+4
132 °C). Proteins were separated by SDS-PAGE and transferred onto membranes. After blocking with
133 5% milk in 0.1% TBS–Tween 20, the membranes were incubated with the corresponding primary
134 antibodies: rabbit anti-human mtArgRS (1:1000, Biorbyt, orb374171), rabbit anti-human COXII
135 (1:500, GeneTex, GTX62145) or rabbit anti-human GAPDH (Cell Signaling Technology, 14C10).
136 Reactive bands were detected using horseradish peroxidase-conjugated secondary antibodies
137 (goat anti-rabbit or goat anti-mouse, 1:10 000, Life Technologies). Blots were imaged using the ECL
138 western blotting substrate (Thermo Fisher Scientific) and Chemidoc XRS+ Molecular Imager (Bio-
139 Rad). Quantification of the band intensities was performed with the Image Lab Software (Bio-Rad).

140

141 **Northern blot and aminoacylation assay**

142 Total RNA was extracted from cultured fibroblasts using Trizol reagent (Thermo Fisher scientific)
143 according to the manufacturer's instructions. To preserve the aminoacylation state the final RNA
144 pellet was re-suspended in 10mM NaOAc at pH 5.0. To investigate the aminoacylation status of mt-
145 tRNAs, 4µg of RNA was separated on long (16cm length) 6.5% polyacrylamide gel (19:1
146 acrylamide:bis-acrylamide) containing 8M urea in 0.1 NaOAc, pH 5.0. The fully deacylated tRNA
147 (dAc) was obtained by incubation of the control RNA at 75°C (pH 9.0) for 15 min. To determine mt-
148 tRNA^{Arg} steady-state levels the samples were run on 10cm gel. Northern hybridization was
149 performed with γ -32P labeled oligonucleotide probes: 5'-GAGTCGAAATCATTCGTTTTG-3' for the
150 mt-tRNA^{Arg} and 5'- GTGGCTGATTGCGTTCAGT-3' for the mt-tRNA^{Ala}. Radioactive signal was
151 detected by PhosphorImager plate using Typhoon scanner and quantified with the ImageQuant
152 v5.0 software (GE Healthcare).

Results

Clinical description

The essential clinical features in our patient are summarized in Supplementary Table. The patient was the first child of non-consanguineous Belgian parents. Family history was unremarkable. He was born at term after an uneventful pregnancy. Birth weight was 3.150 kg (-1 SD), length 50 cm (-1 SD) and head circumference 35 cm (-0.5 SD). After birth slight hypothermia occurred, leading to one day neonatal care, but otherwise physical examination was normal. Very early psychomotor milestones were reported normal, but at the age of 2 to 3 months lack of social interaction, late visual contact and mild hypotonia were noted. No further developmental milestones were reached, he had no speech and showed no real social contact. The patient had no dysmorphic signs at birth, but later presented with bitemporal narrowing, high palate, open mouth, full cheeks, a tented upper lip (Fig. 1A) as well as mild edema of hands (Fig. 1B) and feet. Eye examination showed no visual contact and a pale papilla on both eyes later progressing to optic atrophy. Due to feeding difficulties the child was tube fed. An acquired microcephaly was noted with occipitofrontal circumference (OFC) of 43 cm (-3.3 SD) at the age of 1 year and 46 cm (-3.7 SD) at the age of 3 years. At the last clinical follow-up with 9 years of age, he presented as a bedridden child with profound intellectual disability, axial hypotonia, spastic quadriplegia and significant seizure burden.

First convulsions were witnessed at the age of 6 weeks with lateralized clonic movements of the face, followed by diminished consciousness and eye deviation to one side as well as bilateral clonic movements of the body. It is unclear from the history whether these seizures were already present from birth. Convulsions evolved into therapy-resistant epilepsy with varying seizure types: complex focal seizures (with and without diminished consciousness) with myoclonic jerks and laughing, rhythmic clonic movements of one or both limbs and long-lasting eye deviations with

nystagmus. The patient suffered from daily seizures several times a day with isolated myoclonic spasms and clusters in between.

EEG studies at the age of one to 3 months showed normal background activity without any epileptic activity. Multifocal epileptic activity was seen from the age of 4 months and high voltage slow background activity from the age of 5 months. The EEG did show some signs of hypsarrhythmia and could, because lack of total desynchronization, be described as a modified hypsarrhythmia. The last EEG recording, taken one day before the patient died, demonstrated a picture of status epilepticus with continuous multifocal epileptic activity.

Magnetic resonance imaging (MRI) was performed at the ages of 4.5 months and 7 years. At 4.5 months (Fig. 1C,D), it showed severe cerebral atrophy, destruction of the thalami, and delayed myelination, whereas the cerebellum appeared normal in size. At 7 years (Fig. 1E-G), the cerebellar atrophy was prominent, and microcephaly masked some of the cerebral atrophy. The pons was normal, and the myelination had reached almost a normal appearance.

Thorough metabolic investigations were unremarkable, with the exception of an intermittently raised serum lactate up to 5.3 mmol/l (0.5-2 mmol/l) and an elevated lactate level in the CSF, up to 2.8 mmol/l (<2.5 mmol/l). No abnormalities were seen in the muscle biopsy.

Prior genetic investigations including karyotype and microarray came out normal and mitochondrial DNA mutations were excluded.

The patient died at the age of nearly 12 years due to a respiratory infection.

Molecular findings: *RARS2* mutations and their consequence

Given that the patient presented with symptoms overlapping with those reported in PEHO syndrome, his DNA was first Sanger sequenced to identify variants in the coding regions and splice

sites of *ZNHIT3*. A rare heterozygous c.8C>T, p.Ser3Leu (NM_004773.3) missense variant was identified, but the patient did not have other *ZNHIT3* coding sequence variants. To identify any non-coding variants in *ZNHIT3* locus, the patient was whole genome sequenced. Analysis for rare sequence variants in intronic or UTR regions of *ZNHIT3*, or up- or downstream to *ZNHIT3* did not identify a second variant. No copy number changes overlapping with the *ZNHIT3* locus was identified.

Analysis of the whole genome data was then expanded to all protein coding regions of the genome and splice sites. Whole genome sequence data was produced with mean sequencing coverage of 24.48x, and 98.2%, 95.7% and 74.2% of the genome was covered at least 5x, 10x and 20x, respectively. Analysis of the coding regions from the genome sequence data focused on rare heterozygous and potentially biallelic variants in established disease genes. Analysis of rare heterozygous variants did not yield any likely candidates explaining the patient's disease. Analysis of rare biallelic variants revealed two heterozygous variants in *RARS2* (NM_020320.3; Fig. 2A and B; <https://databases.lovd.nl/shared/individuals/00234052>), a one-bp deletion in exon 10 causing a frameshift and premature termination of translation 16 codons downstream (c.795delA, p.Glu265Aspfs*16) and a missense variant, c.961C>T, p.Leu321Phe, in exon 11. There is one heterozygous carrier for the c.961C>T, p.Leu321Phe variant in the gnomAD (Lek et al., 2016) database (v. 2.0; allele frequency 0.000004), whereas the frameshift variant is absent from the database. The leucine at position 321, located in the catalytic domain of *RARS2*, is highly conserved (Fig. 2B). *In silico* tools SIFT, PolyPhen-2 and MutationTaster predict the c.961C>T, p.Leu321Phe substitution as deleterious. Sanger sequencing confirmed compound heterozygosity of the two mutations in the patient: the c.795delA frameshift mutation was inherited from the mother and the c.961C>T missense mutation from the father (Fig. 2A).

The consequence of the *RARS2* variants was studied on mRNA level in skin fibroblasts of the

224 patient. The frameshift variant in exon 10 resulting in a premature termination codon is predicted
225 to be subjected to nonsense-mediated mRNA decay (NMD) and degradation of the transcript
226 derived from the maternal allele. Indeed, sequencing of *RARS2* cDNA revealed that at position
227 c.961 only the paternal C>T variant was present (Fig. 2C). Western blot analysis of patient
228 fibroblasts revealed that the mtArgRS protein level was reduced to about 50 % of control level (Fig.
229 3A). Northern blot analysis of total RNA from fibroblasts suggested that the steady-state level of
230 mitochondrial tRNA^{Arg} when compared to mitochondrial tRNA^{Ala} may be decreased in patient
231 fibroblasts (Fig. 3B). In patient and control fibroblasts, aminoacylation analysis showed the
232 presence of only aminoacylated mt-tRNA^{Arg}, whereas deacylated mt-tRNA^{Arg} was not detected (Fig.
233 3C). This finding is in agreement with the previous observation (Edvardson et al., 2007), suggesting
234 that in cultured human fibroblasts uncharged mt-tRNA^{Arg} is not stable.

Discussion

We describe a patient compound heterozygous for two novel pathogenic variants in *RARS2*, the gene associated with PCH6. The high conservation of the affected Leu321, the predicted deleteriousness of the Leu321Phe substitution combined with degradation of the transcript derived from the allele with the frameshift variant strongly suggest that these variants are the underlying cause for PCH6 in the patient.

The role of *RARS2* in pontocerebellar hypoplasia is not fully understood with no clear genotype-phenotype correlations. It is though likely that the severity of the disease is dependent of the amount of remaining aminoacylation activity (Konovalova and Tynismaa, 2013). mtArgRS has a fundamental function in mitochondrial protein synthesis, so total loss-of-function mutations are likely to be lethal. Compatible with this notion, mice homozygous for a knock-out allele of *Rars2* are embryonic lethal (International Mouse Phenotyping Consortium; <http://www.mousephenotype.org/data/genes/MGI:1923596#section-associations>). Considering the markedly reduced expression from the frameshift allele, the missense mutant allele is likely to retain some mtArgRS activity in our patient. It has been suggested that due to the leaky nature of the mutations, small amounts of protein synthesis is possible in most tissues, but in high energy demanding cells, such as neurons, the reduced aminoacylation is not sufficient thus causing the symptoms of the disease (Edvardson et al., 2007). Low enzyme activity affects the development of the central nervous system already *in utero* as demonstrated by abnormal brain MRI findings in the neonatal period (e.g. Edvardson et al., 2007; Joseph et al., 2014; Lax et al., 2015). It is also possible that the reduced aminoacylation of tRNA-Arg has bigger effect on specific neuronal types that causes the alterations in brain typical for PCH6. There is also evidence of particular uncharged tRNAs and amino acids working as potential signaling molecules (Dong et al., 2000; Wolfson et al., 2016). Mitochondrial tRNA synthetases may also have non-canonical functions, similarly to their

cytosolic counterparts, in addition to their housekeeping function in protein synthesis, and these may contribute to the pathomechanisms. For example, mtArgRS was recently found to have a specific sub-mitochondrial localization in the membrane, which suggests that it also could have alternative functions (González-Serrano et al., 2018). Regardless of the reason, this high tissue specificity makes functional studies of the disease mechanism challenging.

Including the present patient, 33 patients with PCH6 in 19 families have been described (Supplementary Table). An overview of the key clinical features in the patients is presented in Table 1. Most patients were normal at birth but presented with variable symptoms at early age (hours to 9 months). First presenting features included hypotonia in 15/33 patients and seizures in 16/33 patients. Other early symptoms were poor feeding, lethargy and apneic episodes. All patients were reported to have global developmental delay and the majority presented seizures, the onset varying from 9 hours to several months. Most seizures were intractable myoclonic or tonic-clonic seizures, either focal, or multifocal or generalized. Other common features in the patients include progressive microcephaly, atrophy of cerebellum and cerebrum, as well as elevated lactate levels in blood or CSF. Notably, atrophy of pons was reported to be present in only 12 out of the 25 patients with reported MRI findings, indicating that pons can be normal in PCH6 (Nishri et al., 2016). The phenotype in our patient is similar to that of previously published patients, and presents with all features listed in Table 1, except atrophy of the pons. Of note, as in at least three published patients (Ngoh et al., 2016; Zhang et al., 2018; Luhl et al., 2016), the serum lactate levels in our patient were intermittently raised.

Compatible with a previous report (Rankin et al., 2010), the initial clinical features in our patient including severe intellectual disability, epilepsy, optic atrophy, hypotonia, acquired microcephaly, mild edema of hands and feet, and dysmorphic features pointed to PEHO syndrome. Although the dysmorphic features raised the suspicion of the PEHO syndrome, they may, however, be non-

specific, as many of the dysmorphic facial features are associated with developing microcephaly, extreme floppiness, and edema (Somer, 1993). Contrary to findings in our patient, patients with PEHO syndrome do not show elevated lactate levels in blood or CSF and usually present with neonatal hypotonia (Anttonen et al., 2017). Importantly, the MRI findings in our patient (Fig. 1C-G) were not typical for PEHO syndrome. The supratentorial atrophy was more severe than in a typical PEHO patient. Moreover, the myelination was not delayed to the degree seen in PEHO patients. Characteristic MRI findings including progressive cerebellar atrophy and dysmyelination are essential diagnostic criteria for PEHO syndrome (Anttonen et al., 2017). These typical findings are often disregarded when suggesting a clinical PEHO diagnosis.

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Accession numbers

<https://databases.lovd.nl/shared/individuals/00234052>

Figure Titles and Legends

Figure 1. Phenotypic features in the patient.

A) Facial features of the patient at 7 years of age. Note the open mouth, full cheeks, a tented upper lip and bitemporal narrowing. **B)** The hand shows edema. **C)** In a sagittal T1-weighted cranial magnetic resonance image at the age of 4.5 months cerebellum (arrowhead) and pons (arrow) appear normal in size. **D)** T2-weighted axial image at 4.5 months shows cerebral atrophy. **E & F)** T2-weighted images of the patient at 7 years of age show microcephaly and widespread cerebral atrophy as well as severe cerebellar atrophy (arrowhead in **E**) with widened cerebellar sulci (**F**). The pons (arrow in **E**) as well as the myelination appear normal. **G)** T2-axial slices at 7 years also show atrophy and signal increase of the thalami (open arrowheads).

Figure 2. Two novel PCH6-associated mutations in the *RARS2* gene.

A) Sanger sequencing chromatograms of the proband's (P) and the parents' genomic DNA showing the c.795delA variant inherited from the mother (M) and the c.961C>T variant inherited from the father (F). Positions of variants are indicated with arrowheads. **B)** A schematic picture of the exon-intron structure of *RARS2* and the domain structure of the encoded protein (modified from González-Serrano et al., 2018) showing the locations of the identified mutations and high conservation of the leucine at position 321 affected by the missense substitution. **C)** Sanger sequencing chromatograms of the proband's cDNA showing only the paternal c.961C>T variant (arrowhead) in exon 11 suggesting that the transcript derived from the maternal allele is degraded. 11F denotes forward orientation sequence and 11R reverse orientation

Figure 3. Western blot, northern blot and aminoacylation analysis of the patient fibroblasts.

327 **A)** Steady-state level of mtArgRS protein in patient (P) and control fibroblasts (C1, C2) detected by
328 Western blot. Quantification of the Western blot analysis is shown in the right panel. GAPDH was
329 detected as protein loading control. Data are presented as mean \pm SD. **B)** Northern blot analysis of
330 mt-tRNA^{Arg} levels in patient (P) and control (C1, C2) fibroblasts. Quantification of the northern blot
331 analysis is shown in the lower panel. Mitochondrial tRNA^{Ala} was detected as a loading control.
332 **C)** Aminoacylation assay of mt-tRNA^{Arg} in control (C1, C2) and patient (P) fibroblasts. Mitochondrial
333 tRNA^{Ala} was detected as a loading control. dAC denotes the fully deacylated control tRNA.
334 Experiments in B and C were carried out only once.

Table 1. Overview of clinical features in published PCH6 patients

Feature	<i>n/n^a</i>
Global developmental delay	33/33
Epileptic seizures	24/24
Microcephaly	20/27
MRI findings	
Atrophy of cerebellum	22/25
Atrophy of pons	12/25
Atrophy of cerebrum	18/25
Elevated lactate level in blood or CSF	19/23
Reduced respiratory chain enzyme activity	10/19
Feeding difficulties	17/18
Dysmorphic features	6/8

CSF – cerebrospinal fluid

^a The features are variably reported in the patients.

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539 **Supplemental Data**

540 **Supplementary Table: Phenotypic features in published PCH6 patients**

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